



226749.st25 Replacement Sequence Listing
SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Sogabe, Atsushi
Hattori, Takashi
Nishiya, Yoshiaki
Kawamura, Yoshihisa
- (ii) TITLE OF INVENTION: Creatine Amidinohydrolase, Production
Thereof and Use Thereof
- (iii) NUMBER OF SEQUENCE: 3
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
 - (B) STREET: Two Prudential Plaza, Suite 4900
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: USA
 - (F) ZIP: 60601-6780
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE:
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 10/807,228
 - (B) FILING DATE: 23-MAR-2004
 - (C) CLASSIFICATION: Divisional
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 25435/1996
 - (B) FILING DATE: 13-FEB-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: John Kilyk, Jr.
 - (B) REGISTRATION NUMBER: 30,763
 - (C) REFERENCE/DOCKET NUMBER: 226749
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (312) 616-5600
 - (B) TELEFAX: (312) 616-5700
 - (C) TELEX: 25-3533

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 404 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: protein
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Alcaligenes faecalis*
 - (B) STRAIN: TE3581 (FERM P-14237)
- (ix) FEATURE:
 - (A) NAME/KEY: mat peptide

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 (B) LOCATION: 1 to 404.
 (D) OTHER INFORMATION: protein having creatine amidino-
 hydrolase activity

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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Met Thr Asp Asp Met Leu His Val Met Lys Trp His Asn Gly Glu Lys
 1      5      10      15
Asp Tyr Ser Pro Phe Ser Asp Ala Glu Met Thr Arg Arg Gln Asn Asp
 20      25      30
Val Arg Gly Trp Met Ala Lys Asn Asn Val Asp Ala Ala Leu Phe Thr
 35      40      45
Ser Tyr His Cys Ile Asn Tyr Tyr Ser Gly Trp Leu Tyr Cys Tyr Phe
 50      55      60
Gly Arg Lys Tyr Gly Met Val Ile Asp His Asn Asn Ala Thr Thr Ile
 65      70      75      80
Ser Ala Gly Ile Asp Gly Gly Gln Pro Trp Arg Arg Ser Phe Gly Asp
 85      90      95
Asn Ile Thr Tyr Thr Asp Trp Arg Arg Asp Asn Phe Tyr Arg Ala Val
100      105      110
Arg Gln Leu Thr Thr Gly Ala Lys Arg Ile Gly Ile Glu Phe Asp His
115      120      125
Val Asn Leu Asp Phe Arg Arg Gln Leu Glu Glu Ala Leu Pro Gly Val
130      135      140
Glu Phe Val Asp Ile Ser Gln Pro Ser Met Trp Met Arg Thr Ile Lys
145      150      155      160
Ser Leu Glu Glu Gln Lys Leu Ile Arg Glu Gly Ala Arg Val Cys Asp
165      170      175
Val Gly Gly Ala Ala Cys Ala Ala Ala Ile Lys Ala Gly Val Pro Glu
180      185      190
His Glu Val Ala Ile Ala Thr Thr Asn Ala Met Ile Arg Glu Ile Ala
195      200      205
Lys Ser Phe Pro Phe Val Glu Leu Met Asp Thr Trp Thr Trp Phe Gln
210      215      220
Ser Gly Ile Asn Thr Asp Gly Ala His Asn Pro Val Thr Asn Arg Ile
225      230      235      240
Val Gln Ser Gly Asp Ile Leu Ser Leu Asn Thr Phe Pro Met Ile Phe
245      250      255
Gly Tyr Tyr Thr Ala Leu Glu Arg Thr Leu Phe Cys Asp His Val Asp
260      265      270
Asp Ala Ser Leu Asp Ile Trp Glu Lys Asn Val Ala Val His Arg Arg
275      280      285
Gly Leu Glu Leu Ile Lys Pro Gly Ala Arg Cys Lys Asp Ile Ala Ile
290      295      300
Glu Leu Asn Glu Met Tyr Arg Glu Trp Asp Leu Leu Lys Tyr Arg Ser
305      310      315      320
Phe Gly Tyr Gly His Ser Phe Gly Val Leu Cys His Tyr Tyr Gly Arg
325      330      335
Glu Ala Gly Val Glu Leu Arg Glu Asp Ile Asp Thr Glu Leu Lys Pro
340      345      350
Gly Met Val Val Ser Met Glu Pro Met Val Met Leu Pro Glu Gly Met
355      360      365
Pro Gly Ala Gly Gly Tyr Arg Glu His Asp Ile Leu Ile Val Gly Glu
370      375      380
Asp Gly Ala Glu Asn Ile Thr Gly Phe Pro Phe Gly Pro Glu His Asn
385      390      395      400
Ile Ile Arg Asn
404

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1212 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Alcaligenes faecalis*
(B) STRAIN: TE3581 (FERM P-14237)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1 to 1212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG	ACT	GAC	GAC	ATG	TTG	CAC	GTG	ATG	AAA	TGG	CAC	AAC	GGC	GAG	AAA	48
Met	Thr	Asp	Asp	Met	Leu	His	Val	Met	Lys	Trp	His	Asn	Gly	Glu	Lys	
1				5				10					15			
GAT	TAT	TCG	CCG	TTT	TCG	GAT	GCC	GAG	ATG	ACC	CGC	CGC	CAA	AAC	GAC	96
Asp	Tyr	Ser	Pro	Phe	Ser	Asp	Ala	Glu	Met	Thr	Arg	Arg	Gln	Asn	Asp	
			20					25					30			
GTT	CGC	GGC	TGG	ATG	GCC	AAG	AAC	AAT	GTC	GAT	GCG	GCG	CTG	TTC	ACC	144
Val	Arg	Gly	Trp	Met	Ala	Lys	Asn	Asn	Val	Asp	Ala	Ala	Leu	Phe	Thr	
			35				40					45				
TCT	TAT	CAC	TGC	ATC	AAC	TAC	TAT	TCC	GGC	TGG	CTG	TAC	TGC	TAT	TTC	192
Ser	Tyr	His	Cys	Ile	Asn	Tyr	Tyr	Ser	Gly	Trp	Leu	Tyr	Cys	Tyr	Phe	
	50					55					60					
GGA	CGC	AAG	TAC	GGC	ATG	GTC	ATC	GAC	CAC	AAC	AAC	GCC	ACG	ACG	ATT	240
Gly	Arg	Lys	Tyr	Gly	Met	Val	Ile	Asp	His	Asn	Asn	Ala	Thr	Thr	Ile	
	65				70					75					80	
TCG	GCC	GGC	ATC	GAC	GGC	GGC	CAG	CCC	TGG	CGC	CGC	AGC	TTC	GGC	GAC	288
Ser	Ala	Gly	Ile	Asp	Gly	Gly	Gln	Pro	Trp	Arg	Arg	Ser	Phe	Gly	Asp	
				85					90					95		
AAC	ATC	ACC	TAC	ACC	GAC	TGG	CGC	CGC	GAC	AAT	TTC	TAT	CGC	GCC	GTG	336
Asn	Ile	Thr	Tyr	Thr	Asp	Trp	Arg	Arg	Asp	Asn	Phe	Tyr	Arg	Ala	Val	
			100					105					110			
CGC	CAG	CTG	ACC	ACG	GGC	GCC	AAG	CGC	ATC	GGC	ATC	GAG	TTC	GAC	CAC	384
Arg	Gln	Leu	Thr	Thr	Gly	Ala	Lys	Arg	Ile	Gly	Ile	Glu	Phe	Asp	His	
			115				120					125				
GTC	AAT	CTC	GAC	TTC	CGC	CGC	CAG	CTC	GAG	GAA	GCC	CTA	CCG	GGC	GTC	432
Val	Asn	Leu	Asp	Phe	Arg	Arg	Gln	Leu	Glu	Glu	Ala	Leu	Pro	Gly	Val	
	130					135					140					
GAG	TTC	GTC	GAC	ATC	AGC	CAG	CCC	TCG	ATG	TGG	ATG	CGC	ACC	ATC	AAG	480
Glu	Phe	Val	Asp	Ile	Ser	Gln	Pro	Ser	Met	Trp	Met	Arg	Thr	Ile	Lys	
	145				150					155					160	
TCG	CTC	GAA	GAG	CAG	AAG	CTG	ATC	CGC	GAA	GGC	GCC	CGC	GTG	TGT	GAC	528
Ser	Leu	Glu	Glu	Gln	Lys	Leu	Ile	Arg	Glu	Gly	Ala	Arg	Val	Cys	Asp	
				165					170					175		
GTC	GGC	GGC	GCG	GCC	TGC	GCG	GCT	GCC	ATC	AAG	GCC	GGC	GTG	CCC	GAG	576
Val	Gly	Gly	Ala	Ala	Cys	Ala	Ala	Ala	Ile	Lys	Ala	Gly	Val	Pro	Glu	
			180					185					190			
CAT	GAA	GTG	GCG	ATC	GCC	ACC	ACC	AAT	GCG	ATG	ATC	CGC	GAG	ATC	GCC	624
His	Glu	Val	Ala	Ile	Ala	Thr	Thr	Asn	Ala	Met	Ile	Arg	Glu	Ile	Ala	
			195				200					205				
AAA	TCG	TTC	CCC	TTC	GTG	GAG	CTG	ATG	GAC	ACC	TGG	ACC	TGG	TTC	CAG	672
Lys	Ser	Phe	Pro	Phe	Val	Glu	Leu	Met	Asp	Thr	Trp	Thr	Trp	Phe	Gln	
	210					215					220					
TCG	GGC	ATC	AAC	ACC	GAC	GGC	GCG	CAC	AAT	CCG	GTC	ACC	AAC	CGC	ATC	720
Ser	Gly	Ile	Asn	Thr	Asp	Gly	Ala	His	Asn	Pro	Val	Thr	Asn	Arg	Ile	
	225				230					235					240	
GTG	CAA	TCC	GGC	GAC	ATC	CTT	TCG	CTC	AAC	ACC	TTC	CCG	ATG	ATC	TTC	768
Val	Gln	Ser	Gly	Asp	Ile	Leu	Ser	Leu	Asn	Thr	Phe	Pro	Met	Ile	Phe	

[illegible]